Phyre^2

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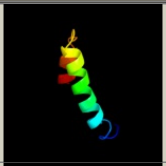
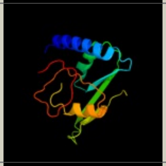
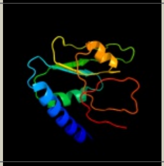
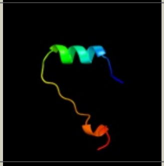
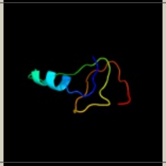
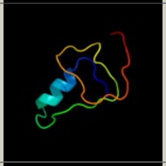
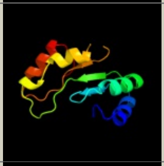
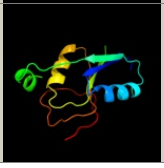
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1ltxA_	Alignment		64.7	14	**PDB header:**transferase/protein binding **Chain:** A: **PDB Molecule:**rab geranylgeranyltransferase alpha subunit; **PDBTitle:** structure of rab escort protein-1 in complex with rab2 geranylgeranyl transferase and isoprenoid
2	d1j7ja_	Alignment		55.9	13	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
3	d1kl7a_	Alignment		55.3	6	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
4	d1g9sa_	Alignment		49.2	12	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
5	c2j5bA_	Alignment		44.6	11	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** structure of the tyrosyl trna synthetase from acanthamoeba2 polyphaga mimivirus complexed with tyrosynol
6	d1a3ca_	Alignment		42.3	10	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
7	d2igba1	Alignment		36.0	15	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
8	c1xuzA_	Alignment		34.3	10	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**polysialic acid capsule biosynthesis protein siac; **PDBTitle:** crystal structure analysis of sialic acid synthase (neub)from2 neisseria meningitidis, bound to mn2+, phosphoenolpyruvate, and n-3 acetyl mannosaminitol
9	c2pjuD_	Alignment		33.9	11	**PDB header:**transcription **Chain:** D: **PDB Molecule:**propionate catabolism operon regulatory protein; **PDBTitle:** crystal structure of propionate catabolism operon2 regulatory protein prpr
10	c1yfzA_	Alignment		33.9	7	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypoxanthine-guanine phosphoribosyltransferase; **PDBTitle:** novel imp binding in feedback inhibition of hypoxanthine-guanine2 phosphoribosyltransferase from thermoanaerobacter tengcongensis
11	d1yfza1	Alignment		33.9	7	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)

12	c3efhB_	Alignment		32.2	8	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ribose-phosphate pyrophosphokinase 1; **PDBTitle:** crystal structure of human phosphoribosyl pyrophosphate2 synthetase 1
13	d1nkta4	Alignment		31.3	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
14	c3o7mD_	Alignment		31.3	7	**PDB header:**transferase **Chain:** D: **PDB Molecule:**hypoxanthine phosphoribosyltransferase; **PDBTitle:** 1.98 angstrom resolution crystal structure of a hypoxanthine-guanine2 phosphoribosyltransferase (hpt-2) from bacillus anthracis str. 'ames3 ancestor'
15	d2zdra2	Alignment		29.0	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**NeuB-like
16	d1ufra_	Alignment		28.8	13	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
17	c3lubE_	Alignment		28.4	23	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**putative creatinine amidohydrolase; **PDBTitle:** crystal structure of putative creatinine amidohydrolase2 (yp_211512.1) from bacteroides fragilis nctc 9343 at 2.11 a3 resolution
18	d1v7za_	Alignment		26.8	17	**Fold:**Creatininase **Superfamily:**Creatininase **Family:**Creatininase
19	d1w30a_	Alignment		25.9	15	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
20	c2q5cA_	Alignment		24.3	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**ntrc family transcriptional regulator; **PDBTitle:** crystal structure of ntrc family transcriptional regulator from2 clostridium acetobutylicum
21	c3cwcB_	Alignment	not modelled	24.1	8	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative glycerate kinase 2; **PDBTitle:** crystal structure of putative glycerate kinase 2 from salmonella2 typhimurium lt2
22	c3no4A_	Alignment	not modelled	24.0	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**creatinine amidohydrolase; **PDBTitle:** crystal structure of a creatinine amidohydrolase (npun_f1913) from2 nostoc punctiforme pcc 73102 at 2.00 a resolution
23	d1d8da_	Alignment	not modelled	22.4	14	**Fold:**alpha-alpha superhelix **Superfamily:**Protein prenylyltransferase **Family:**Protein prenylyltransferase
24	d1hgxa_	Alignment	not modelled	22.4	11	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
25	d1pzma_	Alignment	not modelled	21.0	11	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
26	d1l1qa_	Alignment	not modelled	19.1	8	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
27	d1wgla_	Alignment	not modelled	18.6	11	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**CUE domain
28	c2ps3A_	Alignment	not modelled	18.4	12	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**high-affinity zinc uptake system protein znua; **PDBTitle:** structure and metal binding properties of znua, a2 periplasmic zinc transporter from escherichia coli

29	d1a9xb1	Alignment	not modelled	17.6	15	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Carbamoyl phosphate synthetase, small subunit N-terminal domain **Family:**Carbamoyl phosphate synthetase, small subunit N-terminal domain
30	c2dhyA_	Alignment	not modelled	17.6	10	**PDB header:**immune system **Chain:** A: **PDB Molecule:**cue domain-containing protein 1; **PDBTitle:** solution structure of the cue domain in the human cue2 domain containing protein 1 (cuedc1)
31	c2ov3A_	Alignment	not modelled	17.3	17	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**periplasmic binding protein component of an abc **PDBTitle:** crystal structure of 138-173 znua deletion mutant plus zinc2 bound
32	d1o60a_	Alignment	not modelled	17.1	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I DAHP synthetase
33	c3kb8A_	Alignment	not modelled	17.0	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypoxanthine phosphoribosyltransferase; **PDBTitle:** 2.09 angstrom resolution structure of a hypoxanthine-guanine2 phosphoribosyltransferase (hpt-1) from bacillus anthracis str. 'ames3 ancestor' in complex with gmp
34	d1hrua_	Alignment	not modelled	16.4	20	**Fold:**YrdC/RibB **Superfamily:**YrdC/RibB **Family:**YrdC-like
35	c2ywtA_	Alignment	not modelled	16.1	7	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypoxanthine-guanine phosphoribosyltransferase; **PDBTitle:** crystal structure of hypoxanthine-guanine2 phosphoribosyltransferase with gmp from thermus3 thermophilus hb8
36	d1d7ya2	Alignment	not modelled	15.7	8	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
37	c2o1eB_	Alignment	not modelled	15.4	10	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**ycdh; **PDBTitle:** crystal structure of the metal-dependent lipoprotein ycdh2 from bacillus subtilis, northeast structural genomics3 target sr583
38	d1jcua_	Alignment	not modelled	15.3	21	**Fold:**YrdC/RibB **Superfamily:**YrdC/RibB **Family:**YrdC-like
39	d2h6fa1	Alignment	not modelled	15.3	14	**Fold:**alpha-alpha superhelix **Superfamily:**Protein prenylyltransferase **Family:**Protein prenylyltransferase
40	d1cv8a_	Alignment	not modelled	15.2	11	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Papain-like
41	d1gm5a4	Alignment	not modelled	15.2	10	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
42	c3f6tA_	Alignment	not modelled	15.1	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aspartate aminotransferase; **PDBTitle:** crystal structure of aspartate aminotransferase (e.c. 2.6.1.1)2 (yp_194538.1) from lactobacillus acidophilus ncfm at 2.15 a3 resolution
43	c3dl8B_	Alignment	not modelled	14.9	11	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**protein translocase subunit seca; **PDBTitle:** structure of the complex of aquifex aeolicus secyeg and2 bacillus subtilis seca
44	c2cycB_	Alignment	not modelled	14.3	7	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** crystal structure of tyrosyl-trna synthetase complexed with l-tyrosine2 from pyrococcus horikoshii
45	d2obba1	Alignment	not modelled	14.1	12	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**BT0820-like
46	d1k7ja_	Alignment	not modelled	13.9	25	**Fold:**YrdC/RibB **Superfamily:**YrdC/RibB **Family:**YrdC-like
47	c1keeH_	Alignment	not modelled	13.5	15	**PDB header:**ligase **Chain:** H: **PDB Molecule:**carbamoyl-phosphate synthetase small chain; **PDBTitle:** inactivation of the amidotransferase activity of carbamoyl phosphate2 synthetase by the antibiotic acivicin
48	c3mioA_	Alignment	not modelled	13.3	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3,4-dihydroxy-2-butanone 4-phosphate synthase; **PDBTitle:** crystal structure of 3,4-dihydroxy-2-butanone 4-phosphate synthase2 domain from mycobacterium tuberculosis at ph 6.00
49	d1tksa_	Alignment	not modelled	13.3	14	**Fold:**YrdC/RibB **Superfamily:**YrdC/RibB **Family:**3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
50	c1tnoI_	Alignment	not modelled	13.2	12	**PDB header:**transferase **Chain:** I: **PDB Molecule:**geranylgeranyltransferase type i alpha subunit; **PDBTitle:** rat protein geranylgeranyltransferase type-i complexed with2 a ggpp analog and a kkksktkcvim peptide derived from k-3 ras4b
51	c2advB_	Alignment	not modelled	13.0	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glutaryl 7- aminocephalosporanic acid acylase; **PDBTitle:** crystal structures of glutaryl 7-aminocephalosporanic acid acylase:2 mutational study of activation mechanism

52	d1tuwa_	Alignment	not modelled	12.9	22	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Polyketide synthesis cyclase
53	d1p3qq_	Alignment	not modelled	12.7	17	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**CUE domain
54	d1snna_	Alignment	not modelled	12.5	13	**Fold:**YrdC/RibB **Superfamily:**YrdC/RibB **Family:**3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
55	d1xdfa1	Alignment	not modelled	12.5	18	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**Pathogenesis-related protein 10 (PR10)-like
56	c3m8yC_	Alignment	not modelled	12.4	11	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**phosphopentomutase; **PDBTitle:** phosphopentomutase from bacillus cereus after glucose-1,6-bisphosphate2 activation
57	c1tf2A_	Alignment	not modelled	12.4	11	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**preprotein translocase seca subunit; **PDBTitle:** crystal structure of seca:adp in an open conformation from2 bacillus subtilis
58	c1fcuA_	Alignment	not modelled	12.4	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hyaluronoglucosaminidase; **PDBTitle:** crystal structure (trigonal) of bee venom hyaluronidase
59	d1mn3a_	Alignment	not modelled	12.2	18	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**CUE domain
60	d1fl2a2	Alignment	not modelled	12.1	9	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
61	d1fcqa_	Alignment	not modelled	11.8	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Bee venom hyaluronidase
62	c1pzmB_	Alignment	not modelled	11.7	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**hypoxanthine-guanine phosphoribosyltransferase; **PDBTitle:** crystal structure of hgprt-ase from leishmania tarentolae in complex2 with gmp
63	d1tc1a_	Alignment	not modelled	11.5	9	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
64	d2pjua1	Alignment	not modelled	11.4	11	**Fold:**Chelatase-like **Superfamily:**PrpR receptor domain-like **Family:**PrpR receptor domain-like
65	d1pyfa_	Alignment	not modelled	11.2	8	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
66	d1iuqa_	Alignment	not modelled	11.1	22	**Fold:**Glycerol-3-phosphate (1)-acyltransferase **Superfamily:**Glycerol-3-phosphate (1)-acyltransferase **Family:**Glycerol-3-phosphate (1)-acyltransferase
67	d1g2qa_	Alignment	not modelled	10.9	10	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
68	c2h3oA_	Alignment	not modelled	10.7	9	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**merf; **PDBTitle:** structure of merft, a membrane protein with two trans-2 membrane helices
69	d3pmga2	Alignment	not modelled	10.5	8	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
70	c2ns6A_	Alignment	not modelled	10.3	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mobilization protein a; **PDBTitle:** crystal structure of the minimal relaxase domain of moba2 from plasmid r1162
71	d1ikpa3	Alignment	not modelled	10.3	27	**Fold:**Toxins' membrane translocation domains **Superfamily:**Exotoxin A, middle domain **Family:**Exotoxin A, middle domain
72	d1v71a1	Alignment	not modelled	9.9	11	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
73	c2pe4A_	Alignment	not modelled	9.7	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hyaluronidase-1; **PDBTitle:** structure of human hyaluronidase 1, a hyaluronan hydrolyzing enzyme2 involved in tumor growth and angiogenesis
74	d2pw6a1	Alignment	not modelled	9.7	7	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**LigB-like **Family:**LigB-like
75	d1xrsa_	Alignment	not modelled	9.6	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Cobalamin (vitamin B12)-dependent enzymes **Family:**D-lysine 5,6-aminomutase alpha subunit, KamD
76	c3ktsA_	Alignment	not modelled	9.6	12	**PDB header:**transcriptional regulator **Chain:** A: **PDB Molecule:**glycerol uptake operon antiterminator regulatory protein; **PDBTitle:** crystal structure of glycerol uptake operon antiterminator regulatory2 protein from listeria monocytogenes str. 4b f2365
77	d1iyjb4	Alignment	not modelled	9.5	33	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB

78	c3iraA_	Alignment	not modelled	9.3	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein; **PDBTitle:** the crystal structure of one domain of the conserved protein from2 methanosarcina mazei go1
79	d1nj1a2	Alignment	not modelled	9.1	13	**Fold:**IF3-like **Superfamily:**C-terminal domain of ProRS **Family:**C-terminal domain of ProRS
80	d2aeea1	Alignment	not modelled	8.8	4	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
81	c2lc0A_	Alignment	not modelled	8.8	10	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**putative uncharacterized protein tb39.8; **PDBTitle:** rv0020c_nter structure
82	d2pi8a1	Alignment	not modelled	8.7	11	**Fold:**Double psi beta-barrel **Superfamily:**Barwin-like endoglucanases **Family:**MLTA-like
83	d1vzya2	Alignment	not modelled	8.6	17	**Fold:**HSP33 redox switch-like **Superfamily:**HSP33 redox switch-like **Family:**HSP33 redox switch-like
84	d1mkya3	Alignment	not modelled	8.6	6	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Probable GTPase Der, C-terminal domain **Family:**Probable GTPase Der, C-terminal domain
85	d1k4ia_	Alignment	not modelled	8.5	16	**Fold:**YrdC/RibB **Superfamily:**YrdC/RibB **Family:**3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
86	c2qx5B_	Alignment	not modelled	8.2	29	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**nucleoporin nic96; **PDBTitle:** structure of nucleoporin nic96
87	c3dezA_	Alignment	not modelled	8.2	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** crystal structure of orotate phosphoribosyltransferase from2 streptococcus mutans
88	c2eqaA_	Alignment	not modelled	8.0	21	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**hypothetical protein st1526; **PDBTitle:** crystal structure of the hypothetical sua5 protein from2 sulfolobus tokodaii
89	c2jcyA_	Alignment	not modelled	7.9	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**1-deoxy-d-xylulose 5-phosphate reductoisomerase; **PDBTitle:** x-ray structure of mutant 1-deoxy-d-xylulose 5-phosphate2 reductoisomerase, dxr, rv2870c, from mycobacterium3 tuberculosis
90	c3koxA_	Alignment	not modelled	7.8	16	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**d-ornithine aminomutase e component; **PDBTitle:** crystal structure of ornithine 4,5 aminomutase in complex with 2,4-2 diaminobutyrate (anaerobic)
91	c3cx3A_	Alignment	not modelled	7.8	11	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**lipoprotein; **PDBTitle:** crystal structure analysis of the streptococcus pneumoniae2 adcaii protein
92	c3khsB_	Alignment	not modelled	7.7	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** crystal structure of grouper iridovirus purine nucleoside2 phosphorylase
93	c1r6uB_	Alignment	not modelled	7.6	8	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of an active fragment of human tryptophanyl-trna2 synthetase with cytokine activity
94	d1nj8a2	Alignment	not modelled	7.6	17	**Fold:**IF3-like **Superfamily:**C-terminal domain of ProRS **Family:**C-terminal domain of ProRS
95	c2bnlE_	Alignment	not modelled	7.5	12	**PDB header:**stress-response **Chain:** E: **PDB Molecule:**modulator protein rsbr; **PDBTitle:** the structure of the n-terminal domain of rsbr
96	c3g8rA_	Alignment	not modelled	7.4	12	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**probable spore coat polysaccharide biosynthesis protein e; **PDBTitle:** crystal structure of putative spore coat polysaccharide biosynthesis2 protein e from chromobacterium violaceum atcc 12472
97	c3l6gA_	Alignment	not modelled	7.4	12	**PDB header:**glycine betaine-binding protein **Chain:** A: **PDB Molecule:**betaine abc transporter permease and substrate binding **PDBTitle:** crystal structure of lactococcal opuac in its open conformation
98	d1p17b_	Alignment	not modelled	7.4	9	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
99	c3ie5A_	Alignment	not modelled	7.3	20	**PDB header:**plant protein, biosynthetic protein **Chain:** A: **PDB Molecule:**phenolic oxidative coupling protein hyp-1; **PDBTitle:** crystal structure of hyp-1 protein from hypericum perforatum2 (st john's wort) involved in hypericin biosynthesis